

#8

12/01/92
12:38:01
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Patent Application US/07/864,692

SEQUENCE LISTING

OK

(1) GENERAL INFORMATION:

(i) APPLICANT: Israel, David
Wolfman, Neil M.(ii) TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140-2387

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Tape
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI-5192B

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-876-1170
(B) TELEFAX: 617-876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

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53 ?
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 356..1543
57
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT 60
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63 AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT 120
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65 CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTCACAGC 180
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67 GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG 240
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69 GACATTGGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA 300
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71 ATGGACGTGT CCCCAGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG 358
72 Met
73 1
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75 GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC 406
76 Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
77 5 10 15
78
79 CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC 454
80 Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
81 20 25 30
82
83 GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC 502
84 Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
85 35 40 45
86
87 CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG 550
88 Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
89 50 55 60 65
90
91 AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC 598
92 Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
93 70 75 80
94
95 CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC 646
96 Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His
97 85 90 95
98
99 CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC 694
100 Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His
101 100 105 110
102
103 CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC 742
104 His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr

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	115	120	125	
105				
106				
107	CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC			790
108	Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile			
109	130	135	140	145
110				
111	ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA			838
112	Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu			
113		150	155	160
114				
115	GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA			886
116	Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile			
117		165	170	175
118				
119	AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC			934
120	Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp			
121		180	185	190
122				
123	ACC AGG TTG GTG AAT CAG AAT GCA AGC AGG TGG GAA ACT TTT GAT GTC			982
124	Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp Val			
125		195	200	205
126				
127	ACC CCC GCT GTG ATG CGG TGG ACT GCA CAG GGA CAC GCC AAC CAT GGA			1030
128	Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His Gly			
129	210	215	220	225
130				
131	TTC GTG GTG GAA GTG GCC CAC TTG GAG GAG AAA CAA GGT GTC TCC AAG			1078
132	Phe Val Val Glu Val Ala His Leu Glu Lys Gln Gly Val Ser Lys			
133		230	235	240
134				
135	AGA CAT GTT AGG ATA AGC AGG TCT TTG CAC CAA GAT GAA CAC AGC TGG			1126
136	Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser Trp			
137		245	250	255
138				
139	TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC CAT GAT GGA AAA GGG			1174
140	Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys Gly			
141		260	265	270
142				
143	CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC AAA CAG CGG			1222
144	His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg			
145		275	280	285
146				
147	AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC			1270
148	Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe			
149	290	295	300	305
150				
151	AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC			1318
152	Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His			
153		310	315	320
154				
155	GCC TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG			1366
156	Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu			

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157 i          325          330          335
158
159 AAC TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC      1414
160 Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn
161          340          345          350
162
163 TCT AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC      1462
164 Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile
165          355          360          365
166
167 TCG ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT      1510
168 Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr
169 370          375          380          385
170
171 CAG GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA      1563
172 Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
173          390          395
174
175 CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA      1607
176
177
178 (2) INFORMATION FOR SEQ ID NO:2:
179
180 (i) SEQUENCE CHARACTERISTICS:
181 (A) LENGTH: 396 amino acids
182 (B) TYPE: amino acid
183 (D) TOPOLOGY: linear
184
185 (ii) MOLECULE TYPE: protein
186
187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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189 Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
190 1          5          10          15
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192 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
193          20          25          30
194
195 Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
196          35          40          45
197
198 Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
199          50          55          60
200
201 Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
202 65          70          75          80
203
204 Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
205          85          90          95
206
207 His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
208          100          105          110

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210 His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
211 115 120 125
212
213 Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
214 130 135 140
215
216 Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
217 145 150 155 160
218
219 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
220 165 170 175
221
222 Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
223 180 185 190
224
225 Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp
226 195 200 205
227
228 Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
229 210 215 220
230
231 Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
232 225 230 235 240
233
234 Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
235 245 250 255
236
237 Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
238 260 265 270
239
240 Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
241 275 280 285
242
243 Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
244 290 295 300
245
246 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
247 305 310 315 320
248
249 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
250 325 330 335
251
252 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
253 340 345 350
254
255 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
256 355 360 365
257
258 Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
259 370 375 380
260

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261 Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
262 385 390 395

263

264 (2) INFORMATION FOR SEQ ID NO:3:

265

266 (i) SEQUENCE CHARACTERISTICS:

267 (A) LENGTH: 1954 base pairs

268 (B) TYPE: nucleic acid

269 (C) STRANDEDNESS: double

270 (D) TOPOLOGY: unknown

271

272 (ii) MOLECULE TYPE: DNA (genomic)

273

274

275 (ix) FEATURE:

276 (A) NAME/KEY: CDS

277 (B) LOCATION: 403..1626

278

279

280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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282 CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA 60

283

284 GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG 120

285

286 AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC 180

287

288 ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG 240

289

290 CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC 300

291

292 GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA 360

293

294 TCATGGACTG TTATTATATG CCTTGTTTTT TGTCAAGACA CC ATG ATT CCT GGT 414

295

Met Ile Pro Gly

296

1

297

298 AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC 462

299

299 Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly

300

5

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15

20

301

302 GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC 510

303

303 Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala

304

25

30

35

305

306 GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG 558

307

307 Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu

308

40

45

50

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310 CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC 606

311

311 Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg

312

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313
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315 Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg
316      70                      75                      80
317
318 GAT CTT TAC CGG CTT CAG TCT GGG GAG GAG GAG GAA GAG CAG ATC CAC      702
319 Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu Glu Gln Ile His
320      85                      90                      95                      100
321
322 AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC AGC CGG GCC AAC ACC      750
323 Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser Arg Ala Asn Thr
324                      105                      110                      115
325
326 GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC CCA GGG ACC      798
327 Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile Pro Gly Thr
328                      120                      125                      130
329
330 AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT      846
331 Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile Pro
332                      135                      140                      145
333
334 GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG      894
335 Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln
336                      150                      155                      160
337
338 GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT      942
339 Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile
340                      165                      170                      175                      180
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342 TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC      990
343 Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile
344                      185                      190                      195
345
346 ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG      1038
347 Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp
348                      200                      205                      210
349
350 GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG      1086
351 Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys
352                      215                      220                      225
353
354 CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT      1134
355 Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr
356                      230                      235                      240
357
358 CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA      1182
359 Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln
360                      245                      250                      255                      260
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362 GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC      1230
363 Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly
364                      265                      270                      275

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366 CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT 1278
367 His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg
368 280 285 290
369
370 AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC 1326
371 Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys
372 295 300 305
373
374 CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC 1374
375 Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp
376 310 315 320
377
378 TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC 1422
379 Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp
380 325 330 335 340
381
382 TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT 1470
383 Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
384 345 350 355
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386 GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT 1518
387 Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys
388 360 365 370
389
390 TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG 1566
391 Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu
392 375 380 385
393
394 TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA 1614
395 Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly
396 390 395 400
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398 TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC 1666
399 Cys Gly Cys Arg
400 405
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402 CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC 1726
403
404 ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA 1786
405
406 ATCCCTAAAC ATTACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT 1846
407
408 TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG 1906
409
410 AGTCATTATT TTAAAAAAA AAAAAAACT CTAGAGTCGA CGGAATTC 1954
411
412
413 (2) INFORMATION FOR SEQ ID NO:4:
414
415 (i) SEQUENCE CHARACTERISTICS:
416 (A) LENGTH: 408 amino acids

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417 (B) TYPE: amino acid
418 (D) TOPOLOGY: linear
419
420 (ii) MOLECULE TYPE: protein
421
422 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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424 Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
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427 Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
428 20 25 30
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430 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
431 35 40 45
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433 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
434 50 55 60
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436 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
437 65 70 75 80
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439 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
440 85 90 95
441
442 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
443 100 105 110
444
445 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
446 115 120 125
447
448 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
449 130 135 140
450
451 Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu
452 145 150 155 160
453
454 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
455 165 170 175
456
457 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
458 180 185 190
459
460 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
461 195 200 205
462
463 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
464 210 215 220
465
466 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
467 225 230 235 240
468

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469 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
470 245 250 255
471
472 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
473 260 265 270
474
475 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
476 275 280 285
477
478 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
479 290 295 300
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481 Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
482 305 310 315 320
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484 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
485 325 330 335
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487 Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
488 340 345 350
489
490 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
491 355 360 365
492
493 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
494 370 375 380
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496 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
497 385 390 395 400
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499 Val Val Glu Gly Cys Gly Cys Arg
500 405
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

520 GTGACCGAGC GGCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG TCGGGGCCCG

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522 GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGC GCG ATG CAC GTG CGC TCA CTG      114
523                               Met His Val Arg Ser Leu
524                               1                               5
525
526 CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA CCC CTG TTC      162
527 Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro Leu Phe
528           10                               15                               20
529
530 CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC GAG GTG CAC      210
531 Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu Val His
532           25                               30                               35
533
534 TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG GAG ATG      258
535 Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met
536           40                               45                               50
537
538 CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC CCG CGC CCG      306
539 Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro
540           55                               60                               65                               70
541
542 CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG      354
543 His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu
544           75                               80                               85
545
546 TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC      402
547 Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly
548           90                               95                               100
549
550 TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG      450
551 Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu
552           105                               110                               115
553
554 GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG      498
555 Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met
556           120                               125                               130
557
558 AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC      546
559 Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg
560           135                               140                               145                               150
561
562 TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC CCA GAA GGG      594
563 Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly
564           155                               160                               165
565
566 GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC TAC ATC CGG      642
567 Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile Arg
568           170                               175                               180
569
570 GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG GTG CTC      690
571 Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln Val Leu
572           185                               190                               195

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573
574 CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC GAC AGC CGT      738
575 Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser Arg
576      200                                205                                210
577
578 ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC ATC ACA GCC      786
579 Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr Ala
580 215                                220                                225                                230
581
582 ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG GGC CTG CAG      834
583 Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu Gln
584                                235                                240                                245
585
586 CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG GCG      882
587 Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu Ala
588                                250                                255                                260
589
590 GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC TTC ATG GTG      930
591 Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met Val
592                                265                                270                                275
593
594 GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC CGG TCC ACG      978
595 Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile Arg Ser Thr
596                                280                                285                                290
597
598 GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC AAG AAC CAG      1026
599 Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn Gln
600 295                                300                                305                                310
601
602 GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC AGC GAC CAG      1074
603 Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln
604                                315                                320                                325
605
606 AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG      1122
607 Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu
608                                330                                335                                340
609
610 GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC      1170
611 Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr
612                                345                                350                                355
613
614 TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC      1218
615 Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr
616 360                                365                                370
617
618 AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG      1266
619 Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr
620 375                                380                                385                                390
621
622 GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC      1314
623 Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val
624                                395                                400                                405

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625 -
626 CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA AAC 1362
627 Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn
628 410 415 420
629
630 ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG 1409
631 Met Val Val Arg Ala Cys Gly Cys His
632 425 430
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634 ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC 1448
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637 (2) INFORMATION FOR SEQ ID NO:6:
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639 (i) SEQUENCE CHARACTERISTICS:
640 (A) LENGTH: 431 amino acids
641 (B) TYPE: amino acid
642 (D) TOPOLOGY: linear
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644 (ii) MOLECULE TYPE: protein
645
646 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
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648 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
649 1 5 10 15
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651 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
652 20 25 30
653
654 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
655 35 40 45
656
657 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
658 50 55 60
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660 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
661 65 70 75 80
662
663 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
664 85 90 95
665
666 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
667 100 105 110
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669 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
670 115 120 125
671
672 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
673 130 135 140
674
675 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
676 145 150 155 160

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677
678 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
679 165 170 175
680
681 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
682 180 185 190
683
684 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
685 195 200 205
686
687 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
688 210 215 220
689
690 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
691 225 230 235 240
692
693 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
694 245 250 255
695
696 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
697 260 265 270
698
699 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
700 275 280 285
701
702 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
703 290 295 300
704
705 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
706 305 310 315 320
707
708 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
709 325 330 335
710
711 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
712 340 345 350
713
714 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
715 355 360 365
716
717 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
718 370 375 380
719
720 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
721 385 390 395 400
722
723 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
724 405 410 415
725
726 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
727 420 425 430
728

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729 (2) INFORMATION FOR SEQ ID NO:7:

730

731 (i) SEQUENCE CHARACTERISTICS:

732 (A) LENGTH: 2923 base pairs

733 (B) TYPE: nucleic acid

734 (C) STRANDEDNESS: double

735 (D) TOPOLOGY: circular

736

737 (ii) MOLECULE TYPE: cDNA to mRNA

738

739 (iii) HYPOTHETICAL: NO

740

741 (vi) ORIGINAL SOURCE:

742 (A) ORGANISM: Homo sapiens

743 (F) TISSUE TYPE: Human placenta

744

745 (vii) IMMEDIATE SOURCE:

746 (A) LIBRARY: Stratagene catalog #936203 Human placenta
cDNA library

747 (B) CLONE: BMP6C35

748

749 (viii) POSITION IN GENOME:

750 (C) UNITS: bp

751

752 (ix) FEATURE:

753 (A) NAME/KEY: CDS

754 (B) LOCATION: 160..1701

755

756 (ix) FEATURE:

757 (A) NAME/KEY: mat_peptide

758 (B) LOCATION: 1282..1698

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760 (ix) FEATURE:

761 (A) NAME/KEY: mRNA

762 (B) LOCATION: 1..2923

763

764

765

766 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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768 CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC 60

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770 GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC 120

771

772 GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG 174

773

774 Met Pro Gly Leu Gly

775

776 CGG AGG GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC 222

777

778 Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly Leu Leu Cys Ser Cys

779

780 TGC GGG CCC CCG CCG CTG CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC 270

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781	Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala	
782	-350 -345 -340	
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784	GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG	318
785	Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr	
786	-335 -330 -325	
787		
788	GAG CAG CCG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG	366
789	Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg	
790	-320 -315 -310	
791		
792	CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG	414
793	Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser	
794	-305 -300 -295 -290	
795		
796	GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG	462
797	Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln	
798	-285 -280 -275	
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800	CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG	510
801	Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln	
802	-270 -265 -260	
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804	CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC	558
805	Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro	
806	-255 -250 -245	
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808	CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG	606
809	Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu	
810	-240 -235 -230	
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812	GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA	654
813	Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala	
814	-225 -220 -215 -210	
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816	GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC GCC GCG CAC CCG	702
817	Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro	
818	-205 -200 -195	
819		
820	CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG	750
821	Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala	
822	-190 -185 -180	
823		
824	TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC TTC CTC AAC GAC GCG GAC	798
825	Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp	
826	-175 -170 -165	
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828	ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC	846
829	Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser	
830	-160 -155 -150	
831		
832	CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT	894

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833	Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile	
834	-145 -140 -135 -130	
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836	CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC	942
837	Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
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840	TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT	990
841	Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr	
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844	CAA GTC TTA CAG GAG CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG	1038
845	Gln Val Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu	
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848	GAC ACC CGT GTA GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC	1086
849	Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp	
850	-80 -75 -70	
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852	ATC ACG GCC ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG	1134
853	Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met	
854	-65 -60 -55 -50	
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856	GGG CTT CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC	1182
857	Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro	
858	-45 -40 -35	
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860	CGA GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC	1230
861	Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro	
862	-30 -25 -20	
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864	TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC ACC	1278
865	Phe Met Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr	
866	-15 -10 -5	
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868	AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC TCT ACC	1326
869	Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr	
870	1 5 10 15	
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872	CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT TAC AAC AGC	1374
873	Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser	
874	20 25 30	
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876	AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG TAT GTG AGT TTC	1422
877	Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe	
878	35 40 45	
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880	CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA CCC AAG GGC TAT GCT	1470
881	Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala	
882	50 55 60	
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884	GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC CCA CTC AAC GCA CAC ATG	1518

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885  Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met
886      65                      70                      75
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888  AAT GCA ACC AAC CAC GCG ATT GTG CAG ACC TTG GTT CAC CTT ATG AAC      1566
889  Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn
890      80                      85                      90                      95
891
892  CCC GAG TAT GTC CCC AAA CCG TGC TGT GCG CCA ACT AAG CTA AAT GCC      1614
893  Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala
894      100                      105                      110
895
896  ATC TCG GTT CTT TAC TTT GAT GAC AAC TCC AAT GTC ATT CTG AAA AAA      1662
897  Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys
898      115                      120                      125
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900  TAC AGG AAT ATG GTT GTA AGA GCT TGT GGA TGC CAC TAACTCGAAA      1708
901  Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
902      130                      135                      140
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904  CCAGATGCTG GGGACACACA TTCTGCCTTG GATTCCTAGA TTACATCTGC CTTAAAAAAA      1768
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906  CACGGAAGCA CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT      1828
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908  TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG TAAATGACGT      1888
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910  GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT GTAGCATAAG GTCTGGTAAC      1948
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912  TGCAGAAACA TAACCGTGAA GCTCTTCCTA CCCTCCTCCC CCAAAAACCC ACCAAAATTA      2008
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914  GTTTTAGCTG TAGATCAAGC TATTTGGGGT GTTTGTAGT AAATAGGGAA AATAATCTCA      2068
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916  AAGGAGTTAA ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT      2128
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918  AGATTTTACA GAGAACAGAA ATCGGGGAAG TGGGGGGAAC GCCTCTGTTC AGTTCATTCC      2188
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920  CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG CTCCACGGGG CGCCCTTGTC      2248
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922  TCAGTCATTG CTGTTGTATG TTCGTGCTGG AGTTTTGTTG GTGTGAAAAT ACACTTATTT      2308
923
924  CAGCCAAAAC ATACCATTTC TACACCTCAA TCCTCCATTT GCTGTACTCT TTGCTAGTAC      2368
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926  CAAAAGTAGA CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT      2428
927
928  GAAGGCAGTG CTCACCTCTT CTTTACCAGA ACGGTTCTTT GACCAGCACA TTAACCTCTG      2488
929
930  GACTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT GCCTTTTTTAC TATACAGCAT      2548
931
932  ACCACGCCAC AGGGTTAGAA CCAACGAAGA AAATAAAATG AGGGTGCCCA GCTTATAAGA      2608
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934  ATGGTGTTAG GGGGATGAGC ATGCTGTTTA TGAACGAAA TCATGATTTC CCTGTAGAAA      2668
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936  GTGAGGCTCA GATTAAATTT TAGAATATTT TCTAAATGTC TTTTTCACAA TCATGTGACT      2728
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937-
938 GGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTTGC 2788
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940 ACTTACAGCT TTTTGTGTAATATAAACTA TAATTTATTG TCTATTTTAT ATCTGTTTTG 2848
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942 CTGTGGCGTT GGGGGGGGGG CCGGGCTTTT GGGGGGGGGG GTTTGTTTGG GGGGTGTCGT 2908
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944 GGTGTGGGCG GCGCG 2923
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947 (2) INFORMATION FOR SEQ ID NO:8:
948
949 (i) SEQUENCE CHARACTERISTICS:
950 (A) LENGTH: 513 amino acids
951 (B) TYPE: amino acid
952 (D) TOPOLOGY: linear
953
954 (ii) MOLECULE TYPE: protein
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956 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
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958 Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
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961 Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
962 -355 -350 -345
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964 Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
965 -340 -335 -330
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967 Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
968 -325 -320 -315
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970 Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
971 -310 -305 -300 -295
972
973 Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
974 -290 -285 -280
975
976 His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
977 -275 -270 -265
978
979 Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
980 -260 -255 -250
981
982 Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
983 -245 -240 -235
984
985 Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
986 -230 -225 -220 -215
987
988 Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro

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989      -210      -205      -200
990
991 Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
992      -195      -190      -185
993
994 Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
995      -180      -175      -170
996
997 Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
998      -165      -160      -155
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1000 Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
1001 -150      -145      -140      -135
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1003 Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe
1004      -130      -125      -120
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1006 Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
1007      -115      -110      -105
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1009 Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
1010      -100      -95      -90
1011
1012 Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
1013      -85      -80      -75
1014
1015 Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
1016      -70      -65      -60      -55
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1018 Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
1019      -50      -45      -40
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1021 Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
1022      -35      -30      -25
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1024 Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val
1025      -20      -15      -10
1026
1027 His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
1028      -5      1      5      10
1029
1030 Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
1031      15      20      25
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1033 Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
1034      30      35      40
1035
1036 Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
1037      45      50      55
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1039 Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
1040      60      65      70

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1042 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
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1045 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
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1048 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn
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1051 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys
1052 125 130 135
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1054 His
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1058 (2) INFORMATION FOR SEQ ID NO:9:
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1060 (i) SEQUENCE CHARACTERISTICS:

1061 (A) LENGTH: 2153 base pairs
1062 (B) TYPE: nucleic acid
1063 (C) STRANDEDNESS: double
1064 (D) TOPOLOGY: linear
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1066 (iii) HYPOTHETICAL: NO
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1068 (vi) ORIGINAL SOURCE:

1069 (A) ORGANISM: Homo sapiens
1070 (H) CELL LINE: U2-OS osteosarcoma
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1072 (vii) IMMEDIATE SOURCE:

1073 (A) LIBRARY: U2-OS human osteosarcoma cDNA library
1074 (B) CLONE: U2-16
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1076 (viii) POSITION IN GENOME:

1077 (C) UNITS: bp
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1079 (ix) FEATURE:

1080 (A) NAME/KEY: CDS
1081 (B) LOCATION: 699..2063
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1083 (ix) FEATURE:

1084 (A) NAME/KEY: mat_peptide
1085 (B) LOCATION: 1647..2060
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1087 (ix) FEATURE:

1088 (A) NAME/KEY: mRNA
1089 (B) LOCATION: 1..2153
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1091
1092 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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1098 CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC      180
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1100 GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC      240
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1102 AGGATTTGTT TTGGAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC      300
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1104 TTTGGGAACT ACAGTTTATC AGAAGATCAA CTTTGTCTAA TTCAAATACC AAAGGCCTGA      360
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1110 GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA      540
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1112 TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT      600
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1114 TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT AAGAGGACAA      660
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1117                               Met His Leu Thr Val
1118                               -316-315
1119
1120 TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA      761
1121 Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu
1122   -310                      -305                      -300
1123
1124 GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT      809
1125 Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser
1126 -295                      -290                      -285                      -280
1127
1128 TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG      857
1129 Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg
1130                      -275                      -270                      -265
1131
1132 GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA      905
1133 Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser
1134                      -260                      -255                      -250
1135
1136 CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG      953
1137 Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu
1138 -245                      -240                      -235
1139
1140 GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA      1001
1141 Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val
1142 -230                      -225                      -220
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1144 AGG GCA TCC TTG GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA      1049

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1145 Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro
1146 -215 -210 -205 -200
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1148 GCC TCT CCC AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT 1097
1149 Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr
1150 -195 -190 -185
1151
1152 CCT CTG ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC 1145
1153 Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn
1154 -180 -175 -170
1155
1156 TTT CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA 1193
1157 Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu
1158 -165 -160 -155
1159
1160 AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT CGA 1241
1161 Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe Arg
1162 -150 -145 -140
1163
1164 TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA GCT GAA 1289
1165 Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala Ala Glu
1166 -135 -130 -125 -120
1167
1168 TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA AAT GAA ACA 1337
1169 Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu Asn Glu Thr
1170 -115 -110 -105
1171
1172 ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC ACA AAT AGG GAT 1385
1173 Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr Thr Asn Arg Asp
1174 -100 -95 -90
1175
1176 GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC CAA GCT TTA GAT GTG 1433
1177 Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala Gln Ala Leu Asp Val
1178 -85 -80 -75
1179
1180 GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC AGC AAT CAT TGG GTG ATT 1481
1181 Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser Asn His Trp Val Ile
1182 -70 -65 -60
1183
1184 AAT CCC CAG AAT AAT TTG GGC TTA CAG CTC TGT GCA GAA ACA GGG GAT 1529
1185 Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys Ala Glu Thr Gly Asp
1186 -55 -50 -45 -40
1187
1188 GGA CGC AGT ATC AAC GTA AAA TCT GCT GGT CTT GTG GGA AGA CAG GGA 1577
1189 Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu Val Gly Arg Gln Gly
1190 -35 -30 -25
1191
1192 CCT CAG TCA AAA CAA CCA TTC ATG GTG GCC TTC TTC AAG GCG AGT GAG 1625
1193 Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Ser Glu
1194 -20 -15 -10
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1196 GTA CTT CTT CGA TCC GTG AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC 1673

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1197 Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn
1198 -5 1 5
1199
1200 CGC AAT AAA TCC AGC TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT 1721
1201 Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser Arg Met Ser Ser Val
1202 10 15 20 25
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1204 GGA GAT TAT AAC ACA AGT GAG CAA AAA CAA GCC TGT AAG AAG CAC GAA 1769
1205 Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala Cys Lys Lys His Glu
1206 30 35 40
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1208 CTC TAT GTG AGC TTC CGG GAT CTG GGA TGG CAG GAC TGG ATT ATA GCA 1817
1209 Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
1210 45 50 55
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1212 CCA GAA GGA TAC GCT GCA TTT TAT TGT GAT GGA GAA TGT TCT TTT CCA 1865
1213 Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly Glu Cys Ser Phe Pro
1214 60 65 70
1215
1216 CTT AAC GCC CAT ATG AAT GCC ACC AAC CAC GCT ATA GTT CAG ACT CTG 1913
1217 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
1218 75 80 85
1219
1220 GTT CAT CTG ATG TTT CCT GAC CAC GTA CCA AAG CCT TGT TGT GCT CCA 1961
1221 Val His Leu Met Phe Pro Asp His Val Pro Lys Pro Cys Cys Ala Pro
1222 90 95 100 105
1223
1224 ACC AAA TTA AAT GCC ATC TCT GTT CTG TAC TTT GAT GAC AGC TCC AAT 2009
1225 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn
1226 110 115 120
1227
1228 GTC ATT TTG AAA AAA TAT AGA AAT ATG GTA GTA CGC TCA TGT GGC TGC 2057
1229 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ser Cys Gly Cys
1230 125 130 135
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1232 CAC TAATATTAAA TAATATTGAT AATAACAAAA AGATCTGTAT TAAGGTTTAT 2110
1233 His
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1235
1236 GGCTGCAATA AAAAGCATAC TTTCAGACAA ACAGAAAAAA AAA 2153
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1238
1239 (2) INFORMATION FOR SEQ ID NO:10:
1240
1241 (i) SEQUENCE CHARACTERISTICS:
1242 (A) LENGTH: 454 amino acids
1243 (B) TYPE: amino acid
1244 (D) TOPOLOGY: linear
1245
1246 (ii) MOLECULE TYPE: protein
1247
1248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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1249
1250 Met His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp
1251 -316 -315 -310 -305
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1253 Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn
1254 -300 -295 -290 -285
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1256 His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg
1257 -280 -275 -270
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1259 Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
1260 -265 -260 -255
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1262 Pro Arg Pro Phe Ser Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala
1263 -250 -245 -240
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1265 Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu
1266 -235 -230 -225
1267
1268 Ser Glu Tyr Ser Val Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala
1269 -220 -215 -210 -205
1270
1271 Arg Lys Gly Tyr Pro Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln
1272 -200 -195 -190
1273
1274 Leu Ser Arg Thr Thr Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser
1275 -185 -180 -175
1276
1277 Leu His Asp Thr Asn Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe
1278 -170 -165 -160
1279
1280 Val Asn Leu Val Glu Arg Asp Lys Asp Phe Ser His Gln Arg Arg His
1281 -155 -150 -145
1282
1283 Tyr Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala
1284 -140 -135 -130 -125
1285
1286 Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg
1287 -120 -115 -110
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1289 Phe Glu Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu
1290 -105 -100 -95
1291
1292 Tyr Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala
1293 -90 -85 -80
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1295 Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser
1296 -75 -70 -65
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1298 Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys
1299 -60 -55 -50 -45
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1301 Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu
1302 -40 -35 -30
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1304 Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe
1305 -25 -20 -15
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1307 Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys
1308 -10 -5 1
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1310 Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser
1311 5 10 15 20
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1313 Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala
1314 25 30 35
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1316 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1317 40 45 50
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1319 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
1320 55 60 65
1321
1322 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
1323 70 75 80
1324
1325 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
1326 85 90 95 100
1327
1328 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
1329 105 110 115
1330
1331 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
1332 120 125 130
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1334 Arg Ser Cys Gly Cys His
1335 135
1336
1337

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(F) TISSUE TYPE: Human Heart

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1353
1354 (vii) IMMEDIATE SOURCE:
1355 (A) LIBRARY: Human heart cDNA library stratagene catalog
1356 #936208
1357 (B) CLONE: hh38
1358
1359 (viii) POSITION IN GENOME:
1360 (C) UNITS: bp
1361
1362 (ix) FEATURE:
1363 (A) NAME/KEY: CDS
1364 (B) LOCATION: 8..850
1365
1366 (ix) FEATURE:
1367 (A) NAME/KEY: mat_peptide
1368 (B) LOCATION: 427..843
1369
1370 (ix) FEATURE:
1371 (A) NAME/KEY: mRNA
1372 (B) LOCATION: 1..997
1373
1374
1375 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
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1377 GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC 49
1378 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile
1379 -139 -135 -130
1380
1381 CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG 97
1382 Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val
1383 -125 -120 -115 -110
1384
1385 CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG 145
1386 Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln
1387 -105 -100 -95
1388
1389 GTG GTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 193
1390 Val Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
1391 -90 -85 -80
1392
1393 CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC 241
1394 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val
1395 -75 -70 -65
1396
1397 ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA 289
1398 Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly
1399 -60 -55 -50
1400
1401 CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC GTG GAT CCT GGC 337
1402 Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly
1403 -45 -40 -35 -30
1404

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1405 CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC 385
1406 Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe
1407 -25 -20 -15
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1409 GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG 433
1410 Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg
1411 -10 -5 1
1412
1413 GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG 481
1414 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
1415 5 10 15
1416
1417 CCG CAG GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC 529
1418 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser
1419 20 25 30 35
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1421 CAC GGC CGG CAG GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG 577
1422 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
1423 40 45 50
1424
1425 GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC 625
1426 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
1427 55 60 65
1428
1429 TAT TAC TGT GAG GGG GAG TGC TCC TTC CCG CTG GAC TCC TGC ATG AAC 673
1430 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
1431 70 75 80
1432
1433 GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA 721
1434 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
1435 85 90 95
1436
1437 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC 769
1438 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
1439 100 105 110 115
1440
1441 TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC 817
1442 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
1443 120 125 130
1444
1445 CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC 870
1446 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
1447 135 140
1448
1449 TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC 930
1450
1451 TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG 990
1452
1453 CTTCTGGGAA TTC 1003
1454
1455
1456 (2) INFORMATION FOR SEQ ID NO:12:

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1457-
1458 (i) SEQUENCE CHARACTERISTICS:
1459 (A) LENGTH: 281 amino acids
1460 (B) TYPE: amino acid
1461 (D) TOPOLOGY: linear
1462
1463 (ii) MOLECULE TYPE: protein
1464
1465 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
1466
1467 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
1468 -139 -135 -130 -125
1469
1470 Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser
1471 -120 -115 -110
1472
1473 Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val
1474 -105 -100 -95
1475
1476 Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
1477 -90 -85 -80
1478
1479 Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala
1480 -75 -70 -65 -60
1481
1482 Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg
1483 -55 -50 -45
1484
1485 Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala
1486 -40 -35 -30
1487
1488 Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
1489 -25 -20 -15
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1491 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val
1492 -10 -5 1 5
1493
1494 Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
1495 10 15 20
1496
1497 Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly
1498 25 30 35
1499
1500 Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu
1501 40 45 50
1502
1503 Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
1504 55 60 65
1505
1506 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
1507 70 75 80 85
1508

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1509 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
1510 90 95 100
1511
1512 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
1513 105 110 115
1514
1515 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
1516 120 125 130
1517
1518 Met Val Val Lys Ala Cys Gly Cys His
1519 135 140
1520

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pALBP2-781

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 2724..3071

(ix) FEATURE:

- (A) NAME/KEY: terminator
(B) LOCATION: 3150..3218

(ix) FEATURE:

- (A) NAME/KEY: RBS
(B) LOCATION: 2222..2723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

1550 GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT 60
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1552 CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 120
1553
1554 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT 180
1555
1556 AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT 240
1557
1558 TTGCGGCATT TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 300
1559
1560 CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA 360

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1561
1562 TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC 420
1563
1564 TATGTGGCGC GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC 480
1565
1566 ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG 540
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1568 GCATGACAGT AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 600
1569
1570 ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG 660
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1572 GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG 720
1573
1574 ACGAGCGTGA CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCGCAA CTATTAAGT 780
1575
1576 GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG 840
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1578 TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 900
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1580 GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT 960
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1582 CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC 1020
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1584 AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT 1080
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1586 CATATATACT TTAGATTGAT TTAAAACTTC ATTTTAAATT TAAAAGGATC TAGGTGAAGA 1140
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1588 TCCTTTTTGA TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTT CACTGAGCGT 1200
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1590 CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG CGCGTAATCT 1260
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1592 GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC 1320
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1594 TACCAACTCT TTTTCCGAAG GTAACGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC 1380
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1596 TTCTAGTGTA GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC 1440
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1600 GGTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACGGGGGGTT 1560
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1602 CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG 1620
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1604 AGCATTGAGA AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG 1680
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1606 GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT 1740
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1608 ATAGTCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG 1800
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1610 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC CTGGCCTTTT 1860
1611
1612 GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA 1920

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1613
1614 TTACCGCCTT TGAGTGAGCT GATACCGCTC GCCGCAGCCG AACGACCGAG CGCAGCGAGT 1980
1615
1616 CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC 2040
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1618 CGATTCATTA ATGCAGAATT GATCTCTCAC CTACCAAACA ATGCCCCCCT GCAAAAAATA 2100
1619
1620 AATTCATATA AAAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160
1621
1622 GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA 2220
1623
1624 AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG 2280
1625
1626 GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGC GA TTCCGGATTA GCTGCCAATG 2340
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1628 TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAAC TGCC ACACACCACC AAAGCTAACT 2400
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1630 GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG 2460
1631
1632 GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA 2520
1633
1634 GATTTTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC 2580
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1636 GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA 2640
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1638 GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT 2700
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1640 GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA 2750
1641 Met Gln Ala Lys His Lys Gln Arg Lys
1642 1 5
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1644 CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT 2798
1645 Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
1646 10 15 20 25
1647
1648 GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC 2846
1649 Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala
1650 30 35 40
1651
1652 TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC 2894
1653 Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn
1654 45 50 55
1655
1656 TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT 2942
1657 Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser
1658 60 65 70
1659
1660 AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG 2990
1661 Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser
1662 75 80 85
1663
1664 ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG 3038

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1665 Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln
1666 90 95 100 105
1667
1668 GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA 3088
1669 Asp Met Val Val Glu Gly Cys Gly Cys Arg
1670 110 115
1671
1672 CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC 3148
1673
1674 AGTAATCGTA CAGGGTAGTA CAAATAAAAA AGGCACGTCA GATGACGTGC CTTTTTCTT 3208
1675
1676 GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG 3268
1677
1678 CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA 3328
1679
1680 AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT 3388
1681
1682 GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT 3448
1683
1684 CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC 3508
1685
1686 GCTGACGCGC CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC 3568
1687
1688 GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA 3623
1689
1690
1691 (2) INFORMATION FOR SEQ ID NO:14:
1692
1693 (i) SEQUENCE CHARACTERISTICS:
1694 (A) LENGTH: 115 amino acids
1695 (B) TYPE: amino acid
1696 (D) TOPOLOGY: linear
1697
1698 (ii) MOLECULE TYPE: protein
1699
1700 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
1701
1702 Met Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys
1703 1 5 10 15
1704
1705 Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
1706 20 25 30
1707
1708 Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys
1709 35 40 45
1710
1711 Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
1712 50 55 60
1713
1714 Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
1715 65 70 75 80
1716

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1717 Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn
1718 85 90 95
1719

1720 Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys
1721 100 105 110
1722

1723 Gly Cys Arg
1724 115
1725
1726

1727 (2) INFORMATION FOR SEQ ID NO:15:
1728

1729 (i) SEQUENCE CHARACTERISTICS:
1730 (A) LENGTH: 14 base pairs
1731 (B) TYPE: nucleic acid
1732 (C) STRANDEDNESS: single
1733 (D) TOPOLOGY: linear
1734

1735 (ii) MOLECULE TYPE: DNA (genomic)
1736
1737
1738

1739 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
1740

1741 CATGGGCAGC TGAG
1742

14

1743 (2) INFORMATION FOR SEQ ID NO:16:
1744

1745 (i) SEQUENCE CHARACTERISTICS:
1746 (A) LENGTH: 41 base pairs
1747 (B) TYPE: nucleic acid
1748 (C) STRANDEDNESS: single
1749 (D) TOPOLOGY: linear
1750

1751 (ii) MOLECULE TYPE: DNA (genomic)
1752
1753
1754

1755 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
1756

1757 GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T
1758

41

1759 (2) INFORMATION FOR SEQ ID NO:17:
1760

1761 (i) SEQUENCE CHARACTERISTICS:
1762 (A) LENGTH: 38 base pairs
1763 (B) TYPE: nucleic acid
1764 (C) STRANDEDNESS: single
1765 (D) TOPOLOGY: linear
1766

1767 (ii) MOLECULE TYPE: DNA (genomic)
1768

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1769
1770
1771 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
1772
1773 GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC 38
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1775 (2) INFORMATION FOR SEQ ID NO:18:
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1777 (i) SEQUENCE CHARACTERISTICS:
1778 (A) LENGTH: 31 base pairs
1779 (B) TYPE: nucleic acid
1780 (C) STRANDEDNESS: single
1781 (D) TOPOLOGY: linear
1782
1783 (ii) MOLECULE TYPE: DNA (genomic)
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1785
1786
1787 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
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1789 AATTCACCAT GATTCCTGGT AACCGAATGC T 31
1790
1791 (2) INFORMATION FOR SEQ ID NO:19:
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1793 (i) SEQUENCE CHARACTERISTICS:
1794 (A) LENGTH: 25 base pairs
1795 (B) TYPE: nucleic acid
1796 (C) STRANDEDNESS: single
1797 (D) TOPOLOGY: linear
1798
1799 (ii) MOLECULE TYPE: DNA (genomic)
1800
1801
1802
1803 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
1804
1805 GTGGTACTAA GGACCATTTGG CTTAC 25
1806
1807 (2) INFORMATION FOR SEQ ID NO:20:
1808
1809 (i) SEQUENCE CHARACTERISTICS:
1810 (A) LENGTH: 27 base pairs
1811 (B) TYPE: nucleic acid
1812 (C) STRANDEDNESS: single
1813 (D) TOPOLOGY: linear
1814
1815 (ii) MOLECULE TYPE: DNA (genomic)
1816
1817
1818
1819 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
1820

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1821 CGACCTGCAG CCATGCATCT GACTGTA 27
1822
1823 (2) INFORMATION FOR SEQ ID NO:21:
1824
1825 (i) SEQUENCE CHARACTERISTICS:
1826 (A) LENGTH: 27 base pairs
1827 (B) TYPE: nucleic acid
1828 (C) STRANDEDNESS: single
1829 (D) TOPOLOGY: linear
1830
1831 (ii) MOLECULE TYPE: DNA (genomic)
1832
1833
1834
1835 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
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1837 TGCCTGCAGT TTAATATTAG TGGCAGC 27
1838
1839 (2) INFORMATION FOR SEQ ID NO:22:
1840
1841 (i) SEQUENCE CHARACTERISTICS:
1842 (A) LENGTH: 15 base pairs
1843 (B) TYPE: nucleic acid
1844 (C) STRANDEDNESS: single
1845 (D) TOPOLOGY: linear
1846
1847 (ii) MOLECULE TYPE: DNA (genomic)
1848
1849
1850
1851 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
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1853 CGACCTGCAG CCACC 15
1854
1855 (2) INFORMATION FOR SEQ ID NO:23:
1856
1857 (i) SEQUENCE CHARACTERISTICS:
1858 (A) LENGTH: 81 base pairs
1859 (B) TYPE: nucleic acid
1860 (C) STRANDEDNESS: single
1861 (D) TOPOLOGY: linear
1862
1863 (ii) MOLECULE TYPE: DNA (genomic)
1864
1865
1866
1867 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
1868
1869 TCGACCCACC ATGCCGGGGC TGGGGCGGAG GGCGCAGTGG CTGTGCTGCT GGTGGGGGCT 60
1870
1871 GTGCTGCAGC TGCTGCGGGC C 81
1872

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1873 (2) INFORMATION FOR SEQ ID NO:24:

1874

1875 (i) SEQUENCE CHARACTERISTICS:

1876 (A) LENGTH: 73 base pairs

1877 (B) TYPE: nucleic acid

1878 (C) STRANDEDNESS: single

1879 (D) TOPOLOGY: linear

1880

1881 (ii) MOLECULE TYPE: DNA (genomic)

1882

1883

1884

1885 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

1886

1887 CGCAGCAGCT GCACAGCAGC CCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60

1888

1889 CCGGCATGGT GGG 73

1890

1891 (2) INFORMATION FOR SEQ ID NO:25:

1892

1893 (i) SEQUENCE CHARACTERISTICS:

1894 (A) LENGTH: 11 base pairs

1895 (B) TYPE: nucleic acid

1896 (C) STRANDEDNESS: single

1897 (D) TOPOLOGY: linear

1898

1899 (ii) MOLECULE TYPE: DNA (genomic)

1900

1901

1902

1903 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

1904

1905 TCGACTGGTT T 11

1906

1907 (2) INFORMATION FOR SEQ ID NO:26:

1908

1909 (i) SEQUENCE CHARACTERISTICS:

1910 (A) LENGTH: 9 base pairs

1911 (B) TYPE: nucleic acid

1912 (C) STRANDEDNESS: single

1913 (D) TOPOLOGY: linear

1914

1915 (ii) MOLECULE TYPE: DNA (genomic)

1916

1917

1918

1919 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

1920

1921 CGAAACCAG 9

1922

1923 (2) INFORMATION FOR SEQ ID NO:27:

1924

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1925 (i) SEQUENCE CHARACTERISTICS:
1926 (A) LENGTH: 18 base pairs
1927 (B) TYPE: nucleic acid
1928 (C) STRANDEDNESS: single
1929 (D) TOPOLOGY: linear
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1931 (ii) MOLECULE TYPE: DNA (genomic)
1932
1933
1934
1935 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
1936
1937 TCGACAGGCT CGCCTGCA 18
1938
1939 (2) INFORMATION FOR SEQ ID NO:28:
1940
1941 (i) SEQUENCE CHARACTERISTICS:
1942 (A) LENGTH: 10 base pairs
1943 (B) TYPE: nucleic acid
1944 (C) STRANDEDNESS: single
1945 (D) TOPOLOGY: linear
1946
1947 (ii) MOLECULE TYPE: DNA (genomic)
1948
1949
1950
1951 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
1952
1953 GTCCGAGCGG 10
1954
1955 (2) INFORMATION FOR SEQ ID NO:29:
1956
1957 (i) SEQUENCE CHARACTERISTICS:
1958 (A) LENGTH: 29 base pairs
1959 (B) TYPE: nucleic acid
1960 (C) STRANDEDNESS: single
1961 (D) TOPOLOGY: linear
1962
1963 (ii) MOLECULE TYPE: DNA (genomic)
1964
1965
1966
1967 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
1968
1969 CAGGTCGACC CACCATGCAC GTGCGCTCA 29
1970
1971 (2) INFORMATION FOR SEQ ID NO:30:
1972
1973 (i) SEQUENCE CHARACTERISTICS:
1974 (A) LENGTH: 27 base pairs
1975 (B) TYPE: nucleic acid
1976 (C) STRANDEDNESS: single

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1977 (D) TOPOLOGY: linear
1978
1979 (ii) MOLECULE TYPE: DNA (genomic)
1980
1981
1982
1983 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1984
1985 TCTGTCGACC TCGGAGGAGC TAGTGGC

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/ ,692

DATE: 12/01/92
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S4120

LINE ERROR

ORIGINAL TEXT

29 Wrong application Serial Number
747 Response Exceeds Line Limitations
1356 Response Exceeds Line Limitations

(A) APPLICATION NUMBER: US
cDNA library
#936208



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